

CLUSTAL W (1.83) multiple sequence alignment

gi|4454552|gb|AAD20946.1| = SEQ ID NO:5
gi|1045655|gb|AAC50236.1| = Sequence from Chen et al.

```
gi|4454552|gb|AAD20946.1|      MSGSTQLVAQTWEATEPRYPHSLSYVPQIARTHTDVGLLLEYQHHSRDYA 50
gi|1045655|gb|AAC50236.1|      -----
:  ::                          :  ::                          :  ::
gi|4454552|gb|AAD20946.1|      SHLSPGSIIQPQRRRPSLLSETPQGNERSQHLHPESHSYLPELGKSEM 100
gi|1045655|gb|AAC50236.1|      -----
:  ::                          :  ::                          :  ::
gi|4454552|gb|AAD20946.1|      EFIESKRPRLLELLPDPLLRPSPLIATGQPAGSEDLTKDRSLTGKLEPVSP 150
gi|1045655|gb|AAC50236.1|      -----
:  ::                          :  ::                          :  ::
gi|4454552|gb|AAD20946.1|      PSPHTDPELELVPPRLSKBELIQNDRVDREITWVEQQISKLKKKQQQL 200
gi|1045655|gb|AAC50236.1|      -----
:  ::                          :  ::                          :  ::
gi|4454552|gb|AAD20946.1|      EEEAAKPPEPEKPVSPPIESKHSLSVQITYDENKKAEAAHRILEG LGP 250
gi|1045655|gb|AAC50236.1|      -----
:  ::                          :  ::                          :  ::
gi|4454552|gb|AAD20946.1|      QVELPLYNQPSDTRQYHENIKINQAMRKLLILYFKRRNHARKQWKQKPCQ 300
gi|1045655|gb|AAC50236.1|      -----
:  ::                          :  ::                          :  ::
gi|4454552|gb|AAD20946.1|      RYDQLMEALEKKVERIENNPRRRAKESKVFYEEKQFPPIRKORELQERM 350
gi|1045655|gb|AAC50236.1|      -----
:  ::                          :  ::                          :  ::
gi|4454552|gb|AAD20946.1|      QSRVQSGSGLSMSAARSEHEVSEIIDGLSEQENLEKQNRQLAVIPPMLY 400
gi|1045655|gb|AAC50236.1|      -----
:  ::                          :  ::                          :  ::
gi|4454552|gb|AAD20946.1|      DADQQRIFINMGLMADPMKVYKQVMNMWSEQEKETFREKFMQHPKN 450
gi|1045655|gb|AAC50236.1|      -----
:  ::                          :  ::                          :  ::
gi|4454552|gb|AAD20946.1|      FGLIASFLERKTVAECVLYYYLTKNKNYKSLVRRSYRRRGKSQQQQQQQ 500
gi|1045655|gb|AAC50236.1|      -----
:  ::                          :  ::                          :  ::
```

DLNR_282270.1

2

gi 4454552 gb AAD20946.1	SGLPFFVPRREVITKASPHADPDSAFSYAPPGHPLPLGLHDTARPVLPRPP 1100
gi 1045655 gb AAC50236.1	SGLPFFVPRREVITKASPHADPDSAFSYAPPGHPLPLGLHDTARPVLPRPP 78

gi 4454552 gb AAD20946.1	TISNPPPLISSAKHPSVLERQIGAIISQGSVQLHVPYSEHAKAPVGPVTM 1150
gi 1045655 gb AAC50236.1	TISNPPPLISSAKHPSVLERQIGAIISQGSVQLHVPYSEHAKAPVGPVTM 128

gi 4454552 gb AAD20946.1	GLPLPMDPKKLAPFSGVKQEQLSPRGQAGPPESLGVPTAQEASVLRGTAL 1200
gi 1045655 gb AAC50236.1	GLPLPMDPKKLAPFSGVKQEQLSPRGQAGPPESLGVPTAQEASVLRGTAL 178

gi 4454552 gb AAD20946.1	GSVPGGSITKGIPTSTVPSDSAITYRGSITHGTPADVLYKGTITRIIGED 1250
gi 1045655 gb AAC50236.1	GSVPGGSITKGIPTSTVPSDSAITYRGSITHGTPADVLYKGTITRIIGED 228

gi 4454552 gb AAD20946.1	SPSRIDRGREDSLPKGHVIYEGKKGHVLSYEGGMSVTQCSKEDGRSSGP 1300
gi 1045655 gb AAC50236.1	SPSRIDRGREDSLPKGHVIYEGKKGHVLSYEGGMSVTQCSKEDGRSSGP 278

gi 4454552 gb AAD20946.1	PHETAAPKRTYDMWEGRVGRAISSASIEGLMGRATPPERHSPHLKEQHH 1350
gi 1045655 gb AAC50236.1	PHETAAPKRTYDMWEGRVGRAISSASIEGLMGRATPPERHSPHLKEQHH 328

gi 4454552 gb AAD20946.1	IRGSITQGI PRSYVEAQEDYLRREAKLLKREGTTPPPPPSRDLTEAYKTQ 1400
gi 1045655 gb AAC50236.1	IRGSITQGI PRSYVEAQEDYLRREAKLLKREGTTPPPPPSRDLTEAYKTQ 378

gi 4454552 gb AAD20946.1	ALGPLKLKPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGS 1450
gi 1045655 gb AAC50236.1	ALGPLKLKPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGS 428

gi 4454552 gb AAD20946.1	ITQGTPLKYDTGASTTGSKKHDVRSLSIGSPGTTPPVHPLDVMDARALE 1500
gi 1045655 gb AAC50236.1	ITQGTPLKYDTGASTTGSKKHDVRSLSIGSPGTTPPVHPLDVMDARALE 478

gi 4454552 gb AAD20946.1	RACYEESLKSRRPCTASSSGSIARGAPVIVPELKGPRQSPLTYEDHGAPF 1550
gi 1045655 gb AAC50236.1	RACYEESLKSRRPCTASSSGSIARGAPVIVPELKGPRQSPLTYEDHGAPF 528

gi 4454552 gb AAD20946.1	AGHLPRGSPVTWREPTPLQEGSLSSSKASQDRKLTSTPREIAKSPHSTV 1600
gi 1045655 gb AAC50236.1	AGHLPRGSPVTWREPTPLQEGSLSSSKASQDRKLTSTPREIAKSPHSTV 578

gi 4454552 gb AAD20946.1	PEHHPFISPYEHLRLRGVGDLYRSHIFLADPDTSPRGIPLDAAAAY 1650
gi 1045655 gb AAC50236.1	PEHHPFISPYEHLRLRGVGDLYRSHIFLADPDTSPRGIPLDAAAAY 628

gi 4454552 gb AAD20946.1	LPRHLAPNPTYPHLYPPYLIRGYPDFALENRQTIINDYITTSQQMHNTA 1700
gi 1045655 gb AAC50236.1	LPRHLAPNPTYPHLYPPYLIRGYPDFALENRQTIINDYITTSQQMHNTA 678

gi 4454552 gb AAD20946.1	TAMQADMLRGLSPRESSLALNYAAGPRGIIDLQVPHLPVLVPPPTGT 1750
gi 1045655 gb AAC50236.1	TAMQADMLRGLSPRESSLALNYAAGPRGIIDLQVPHLPVLVPPPTGT 728

gi 4454552 gb AAD20946.1	PATAMDRLAYLPTAPQPFSSRHSSPLSPGGPHTLTKPTTSSSERDR 1800
gi 1045655 gb AAC50236.1	PATAMDRLAYLPTAPQPFSSRHSSPLSPGGPHTLTKPTTSSSERDR 778

gi 4454552 gb AAD20946.1	DREDRDREREKSILTSTTVEHAPIWRPGTEQSSGSSGGGGSSSR 1850
gi 1045655 gb AAC50236.1	DREDRDREREKSILTSTTVEHAPIWRPGTEQSSGSSGGGGSSSR 828

gi 4454552 gb AAD20946.1	PASHSHAHQHSPISPRTODALQORPSVLHNTGMKGIIITAVEPSKPTVLR 1900
gi 1045655 gb AAC50236.1	PASHSHAHQHSPISPRTODALQORPSVLHNTGMKGIIITAVEPSKPTVLR 878

gi 4454552 gb AAD20946.1	TSTSSPVRPAATFPATHCPGLGTLGVYPTLMEPVLLPKEAPRVARPER 1950
gi 1045655 gb AAC50236.1	TSTSSPVRPAATFPATHCPGLGTLGVYPTLMEPVLLPKEAPRVARPER 928

gi 4454552 gb AAD20946.1	PRADTGHAFIAPKPPARSGLPEPASSPSKGSERPLVPPVSGHATIARTPAK 2000
gi 1045655 gb AAC50236.1	PRADTGHAFIAPKPPARSGLPEPASSPSKGSERPLVPPVSGHATIARTPAK 978

gi 4454552 gb AAD20946.1	NLAPHASDPDPAPPASASDPHREKTSQKPFISIQELRLSLGYHGSSYSP 2050
gi 1045655 gb AAC50236.1	NLAPHASDPDPAPPASASDPHREKTSQKPFISIQELRLSLGYHGSSYSP 1028

gi 4454552 gb AAD20946.1	EGVEPVSPVSSPLTHDKGLPKHLEELDKSHLEGLRPKQPGPVKLGEA 2100
gi 1045655 gb AAC50236.1	EGVEPVSPVSSPLTHDKGLPKHLEELDKSHLEGLRPKQPGPVKLGEA 1078

gi 4454552 gb AAD20946.1	AHLPHLRPLPESQPSPLLOTPAGVKGHQVRVTTAQHISEVITQDYTRH 2150
gi 1045655 gb AAC50236.1	AHLPHLRPLPESQPSPLLOTPAGVKGHQVRVTTAQHISEVITQDYTRH 1128

```

*****
HPQOLSAPLPAPLYSFPGASCPVLDLRRPSPDLYLPPPDHGAPARGSPHS 2200
HPQOLSAPLPAPLYSFPGASCPVLDLRRPSPDLYLPPPDHGAPARGSPHS 1178
*****
EGGKRSPENKTSVLGGEDGIEPVSPRGWTEPGHRSVAVYPLLRYDGE 2250
EGGKRSPENKTSVLGGEDGIEPVSPRGWTEPGHRSVAVYPLLRYDGE 1228
*****
QTEPSRMGSKSPGNTSQPPAFFSKLTSNSAMVSKKQEIINKKLNTHNRN 2300
QTEPSRMGSKSPGNTSQPPAFFSKLTSNSAMVSKKQEIINKKLNTHNRN 1278
*****
EPEYNISQPGTEIFNMPAITGTGLMTRYRSQAVQEHASTNMGLEAITRKAL 2350
EPEYNISQPGTEIFNMPAITGTGLMTRYRSQAVQEHASTNMGLEAITRKAL 1328
*****
MGKYDQWBEESPPLSANAFNPLNASASLPAAMPITAADGRSDHTLTSPGGG 2400
MGKYDQWBEESPPLSANAFNPLNASASLPAAMPITAADGRSDHTLTSPGGG 1378
*****
GKAKVSGRPSRKAQSPAGLASGDRPPSVSVHSEGDGDCNRRTPLTNRVW 2450
GKAKVSGRPSRKAQSPAGLASGDRPPSVSVHSEGDGDCNRRTPLTNRVW 1428
*****
EDRPSSAGSTPPYNPLIMRLQAGVNASPPPGILPAGSGPLAGPHHAWDE 2500
EDRPSSAGSTPPYNPLIMRLQAGVNASPPPGILPAGSGPLAGPHHAWDE 1478
*****
EPKPLLCQYETLSDSE 2517
EPKPLLCQYETLSDSE 1495
*****

```